

SEQUENCE LISTING

<110> Wu, Wenping
 Lange, Lene
 Skovlund, Dominique Aubert
 Liu, Ye

<120> Polypeptides having Cellobiohydrlase II Activity and
 Polynucleotides Encoding Same

<130> 10377.204-US

<160> 36

<170> PatentIn version 3.3

<210> 1

<211> 1731

<212> DNA

<213> Chaetomium thermophilum NP000980

<220>

<221> CDS

<222> (63)..(1493)

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 Met Ala Lys Gln Leu Leu Leu Thr Ala Ala Leu Ala Ala Thr Ser
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ctg gct gcc cct ctc ctt gag gag cgc cag agc tgc tcc tcc gtc tgg 155
 Leu Ala Ala Pro Leu Leu Glu Glu Arg Gln Ser Cys Ser Ser Val Trp
 20 25 30

ggt caa tgc ggt ggc atc aat tac aac ggc ccg acc tgc tgc cag tcc 203
 Gly Gln Cys Gly Gly Ile Asn Tyr Asn Gly Pro Thr Cys Cys Gln Ser
 35 40 45

ggc agt gtt tgc act tac ctg aat gac tgg tac agc cag tgc att ccc 251
 Gly Ser Val Cys Thr Tyr Leu Asn Asp Trp Tyr Ser Gln Cys Ile Pro
 50 55 60

ggt cag gct cag ccc ggc acg act agc acc acg gct cgg acc acc agc / 299
 Gly Gln Ala Gln Pro Gly Thr Thr Ser Thr Thr Ala Arg Thr Thr Ser
 65 70 75

acc agc acc acc agc act tcg tcg gtc cgc ccg acc acc tcg aat acc 347
 Thr Ser Thr Thr Ser Thr Ser Ser Val Arg Pro Thr Thr Ser Asn Thr
 80 85 90 95

cct gtg acg act gct ccc ccg acg acc acc atc ccg ggc ggc gcc tcg 395
 Pro Val Thr Thr Ala Pro Pro Thr Thr Thr Ile Pro Gly Gly Ala Ser
 100 105 110

agc acg gcc agc tac aac ggc aac ccg ttt tcg ggt gtt caa ctt tgg Ser Thr Ala Ser Tyr Asn Gly Asn Pro Phe Ser Gly Val Gln Leu Trp 115 120 125	443
gcc aac acc tac tac tcg tcc gag gtg cac act ttg gcc atc ccc agc Ala Asn Thr Tyr Tyr Ser Ser Glu Val His Thr Leu Ala Ile Pro Ser 130 135 140	491
ttg tct cct gag ctg gct gcc aag gcc gcc aag gtc gct gag gtt ccc Leu Ser Pro Glu Leu Ala Ala Lys Ala Ala Lys Val Ala Glu Val Pro 145 150 155	539
agc ttc cag tgg ctc gac cgc aat gtg act gtt gac act ctc ttc tcc Ser Phe Gln Trp Leu Asp Arg Asn Val Thr Val Asp Thr Leu Phe Ser 160 165 170 175	587
ggc act ctt gcc gaa atc cgc gcc gcc aac cag cgc ggt gcc aac ccg Gly Thr Leu Ala Glu Ile Arg Ala Ala Asn Gln Arg Gly Ala Asn Pro 180 185 190	635
cct tat gcc ggc att ttc gtg gtt tat gac tta cca gac cgt gat tgc Pro Tyr Ala Gly Ile Phe Val Val Tyr Asp Leu Pro Asp Arg Asp Cys 195 200 205	683
gcg gct gct gct tcg aac ggc gag tgg tct atc gcc aac aat ggt gcc Ala Ala Ala Ala Ser Asn Gly Glu Trp Ser Ile Ala Asn Asn Gly Ala 210 215 220	731
aac aac tac aag cgc tac atc gac cgg atc cgt gag ctc ctt atc cag Asn Asn Tyr Lys Arg Tyr Ile Asp Arg Ile Arg Glu Leu Leu Ile Gln 225 230 235	779
tac tcc gat atc cgc act att ctg gtc att gaa cct gat tcc ctg gcc Tyr Ser Asp Ile Arg Thr Ile Leu Val Ile Glu Pro Asp Ser Leu Ala 240 245 250 255	827
aac atg gtc acc aac atg aac gtc cag aag tgc tcg aac gct gcc tcc Asn Met Val Thr Asn Met Asn Val Gln Lys Cys Ser Asn Ala Ala Ser 260 265 270	875
act tac aag gag ctt act gtc tat gcc ctc aaa cag ctc aat ctt cct Thr Tyr Lys Glu Leu Thr Val Tyr Ala Leu Lys Gln Leu Asn Leu Pro 275 280 285	923
cac gtt gcc atg tac atg gat gct ggc cac gct ggc tgg ctt ggc tgg His Val Ala Met Tyr Met Asp Ala Gly His Ala Gly Trp Leu Gly Trp 290 295 300	971
ccc gcc aac atc cag cct gct gct gag ctc ttt gct caa atc tac cgc Pro Ala Asn Ile Gln Pro Ala Ala Glu Leu Phe Ala Gln Ile Tyr Arg 305 310 315	1019
gac gct ggc agg ccc gct gct gtc cgc ggt ctt gcg acc aac gtt gcc Asp Ala Gly Arg Pro Ala Ala Val Arg Gly Leu Ala Thr Asn Val Ala 320 325 330 335	1067
aac tac aat gct tgg tcg atc gcc agc cct ccg tcc tac acc tct cct	1115

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Asn	Pro	Asn	Tyr	Asp	Glu	Lys	His	Tyr	Ile	Glu	Ala	Phe	Ala	Pro	Leu		
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aac	ggc	aag	cag	ccc	act	ggc	cag	ctt	gaa	tgg	ggt	cac	tgg	tgc	aat	1259	
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gtc	aag	gga	act	ggc	ttc	ggt	gtg	cgc	cct	act	gct	aac	act	ggg	cat	1307	
Val	Lys	Gly	Thr	Gly	Phe	Gly	Val	Arg	Pro	Thr	Ala	Asn	Thr	Gly	His		
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gaa	ctt	gtt	gat	gct	ttc	gtg	tgg	gtc	aag	ccc	ggt	ggc	gag	tcc	gac	1355	
Glu	Leu	Val	Asp	Ala	Phe	Val	Trp	Val	Lys	Pro	Gly	Gly	Glu	Ser	Asp		
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ggc	acc	agt	gcg	gac	acc	agc	gct	gct	cgt	tat	gac	tat	cac	tgc	ggc	1403	
Gly	Thr	Ser	Ala	Asp	Thr	Ser	Ala	Ala	Arg	Tyr	Asp	Tyr	His	Cys	Gly		
			435					440					445				
ctt	tcc	gac	gca	ctg	act	ccg	gcg	cct	gag	gct	ggc	caa	tgg	ttc	cag	1451	
Leu	Ser	Asp	Ala	Leu	Thr	Pro	Ala	Pro	Glu	Ala	Gly	Gln	Trp	Phe	Gln		
		450					455					460					
gct	tat	ttc	gaa	cag	ctg	ctc	atc	aat	gcc	aac	cct	ccg	ctc			1493	
Ala	Tyr	Phe	Glu	Gln	Leu	Leu	Ile	Asn	Ala	Asn	Pro	Pro	Leu				
	465				470					475							
tgaacggaag	cggagataacc	ggaaggcggg	gagaagagcg	gaattcaagt	ctgcttatca	1553											
aaatccactc	accaagtggg	ttaaagcgga	tttatacatc	tgagaaacaa	cctgctttaa	1613											
actcttcttg	tacatatctc	acttcgagac	gtgcctcttt	ctcaggagca	ctgtagatac	1673											
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			20					25					30		

Gln Cys Gly Gly Ile Asn Tyr Asn Gly Pro Thr Cys Cys Gln Ser Gly
 35 40 45

Ser Val Cys Thr Tyr Leu Asn Asp Trp Tyr Ser Gln Cys Ile Pro Gly
 50 55 60

Gln Ala Gln Pro Gly Thr Thr Ser Thr Thr Ala Arg Thr Thr Ser Thr
 65 70 75 80

Ser Thr Thr Ser Thr Ser Ser Val Arg Pro Thr Thr Ser Asn Thr Pro
 85 90 95

Val Thr Thr Ala Pro Pro Thr Thr Thr Ile Pro Gly Gly Ala Ser Ser
 100 105 110

Thr Ala Ser Tyr Asn Gly Asn Pro Phe Ser Gly Val Gln Leu Trp Ala
 115 120 125

Asn Thr Tyr Tyr Ser Ser Glu Val His Thr Leu Ala Ile Pro Ser Leu
 130 135 140

Ser Pro Glu Leu Ala Ala Lys Ala Ala Lys Val Ala Glu Val Pro Ser
 145 150 155 160

Phe Gln Trp Leu Asp Arg Asn Val Thr Val Asp Thr Leu Phe Ser Gly
 165 170 175

Thr Leu Ala Glu Ile Arg Ala Ala Asn Gln Arg Gly Ala Asn Pro Pro
 180 185 190

Tyr Ala Gly Ile Phe Val Val Tyr Asp Leu Pro Asp Arg Asp Cys Ala
 195 200 205

Ala Ala Ala Ser Asn Gly Glu Trp Ser Ile Ala Asn Asn Gly Ala Asn
 210 215 220

Asn Tyr Lys Arg Tyr Ile Asp Arg Ile Arg Glu Leu Leu Ile Gln Tyr
 225 230 235 240

Ser Asp Ile Arg Thr Ile Leu Val Ile Glu Pro Asp Ser Leu Ala Asn
 245 250 255

Met Val Thr Asn Met Asn Val Gln Lys Cys Ser Asn Ala Ala Ser Thr
 260 265 270

Tyr Lys Glu Leu Thr Val Tyr Ala Leu Lys Gln Leu Asn Leu Pro His
 275 280 285

Val Ala Met Tyr Met Asp Ala Gly His Ala Gly Trp Leu Gly Trp Pro
 290 295 300

Ala Asn Ile Gln Pro Ala Ala Glu Leu Phe Ala Gln Ile Tyr Arg Asp
 305 310 315 320

Ala Gly Arg Pro Ala Ala Val Arg Gly Leu Ala Thr Asn Val Ala Asn
 325 330 335

Tyr Asn Ala Trp Ser Ile Ala Ser Pro Pro Ser Tyr Thr Ser Pro Asn
 340 345 350

Pro Asn Tyr Asp Glu Lys His Tyr Ile Glu Ala Phe Ala Pro Leu Leu
 355 360 365

Arg Asn Gln Gly Phe Asp Ala Lys Phe Ile Val Asp Thr Gly Arg Asn
 370 375 380

Gly Lys Gln Pro Thr Gly Gln Leu Glu Trp Gly His Trp Cys Asn Val
 385 390 395 400

Lys Gly Thr Gly Phe Gly Val Arg Pro Thr Ala Asn Thr Gly His Glu
 405 410 415

Leu Val Asp Ala Phe Val Trp Val Lys Pro Gly Gly Glu Ser Asp Gly
 420 425 430

Thr Ser Ala Asp Thr Ser Ala Ala Arg Tyr Asp Tyr His Cys Gly Leu
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Ser Asp Ala Leu Thr Pro Ala Pro Glu Ala Gly Gln Trp Phe Gln Ala
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 <213> Myceliophthora thermophila

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 <223> n is a, c, g, or t

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 ccgcccgtct ccagccctcg tgaccagcat tcccggcgggt gcgacctcca cggcgagcta 180
 ctctggcaac cccttctcgg gcgtccggct cttcgccaac gactactaca ggtccgaggt 240
 ccacaatctc gccattccta gcatgactgg tactctggcg gctcaaggct tccgccgtcg 300
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 ggtccagact ctgtaccag gtccgggctc tcaataaggc acggtgaaca atcctaccn 420
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 aacggygagt ttctgattgc aaacggcggc gccgccaact acaggagcta catcgacgct 540
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 taccacgagt tgaccgtgta cgcgctcaag cagctgaacc tgcccaacgt cgccatgtat 720
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 ctgtttgccg gcatctacaa tgatgccggc aagccggctg ccgtccgcgg cctggccact 840
 aacgtcgcca actacaacgc ctggagcatc gcttcggccc cgtcgtacac gtcggctaac 900
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acggggccacg agctggtcga tgcctttgtc tgggtcaagc ccggcggcga gtccgacggc 1140
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Leu Ser Thr Thr Pro Pro Pro Val Ser Ser Pro Arg Asp Gln His Ser
35 40 45

Arg Arg Cys Asp Leu His Gly Glu Leu Leu Trp Gln Pro Leu Leu Gly
50 55 60

Arg Pro Ala Leu Arg Gln Arg Leu Leu Gln Val Arg Gly Pro Gln Ser
65 70 75 80

Arg His Ser His Asp Trp Tyr Ser Gly Gly Ser Arg Leu Pro Pro Ser
85 90 95

Arg Glu Val Pro Ser Phe Gln Trp Leu Asp Thr Glu Arg Ala Leu Ile
100 105 110

Arg His Pro Asp Gly Pro Asp Ser Val Pro Arg Ser Gly Leu Ser Ile
115 120 125

Arg His Gly Glu Gln Ser Tyr Pro Tyr Ala Ala Gln Leu Val Val Tyr
130 135 140

Asp Leu Pro Asp Arg Asp Cys Ala Ala Ala Ala Ser Asn Gly Glu Phe
145 150 155 160

Ser Ile Ala Asn Gly Gly Ala Ala Asn Tyr Arg Ser Tyr Ile Asp Ala
165 170 175

Ile Arg Lys His Ile Ile Glu Tyr Ser Asp Ile Arg Ile Ile Leu Val
180 185 190

Ile Glu Pro Asp Ser Met Ala Asn Met Val Thr Asn Met Asn Val Ala
195 200 205

Lys Cys Ser Asn Ala Ala Ser Thr Tyr His Glu Leu Thr Val Tyr Ala
210 215 220

Leu Lys Gln Leu Asn Leu Pro Asn Val Ala Met Tyr Leu Asp Ala Gly
225 230 235 240

His Ala Gly Trp Leu Gly Trp Pro Ala Asn Ile Gln Pro Ala Ala Glu
245 250 255

Leu Phe Ala Gly Ile Tyr Asn Asp Ala Gly Lys Pro Ala Ala Val Arg
260 265 270

Gly Leu Ala Thr Asn Val Ala Asn Tyr Asn Ala Trp Ser Ile Ala Ser
275 280 285

Ala Pro Ser Tyr Thr Ser Ala Asn Pro Asn Tyr Asp Glu Lys His Tyr
290 295 300

Ile Glu Ala Phe Ser Pro Leu Leu Asn Ser Ala Gly Phe Pro Ala Arg
305 310 315 320

Phe Ile Val Asp Thr Gly Arg Asn Gly Lys Gln Pro Thr Gly Gln Gln
325 330 335

Gln Trp Gly Asp Trp Cys Asn Val Lys Gly Thr Gly Phe Gly Val Arg
340 345 350

Pro Thr Ala Asn Thr Gly His Glu Leu Val Asp Ala Phe Val Trp Val
355 360 365

Lys Pro Gly Gly Glu Ser Asp Gly Thr Ser Asp Thr Ser Ala Ala Arg
370 375 380

Tyr Asp Tyr His Cys Gly Leu Ser Asp Ala Leu Gln Pro Ala Pro Glu

385 390 395 400

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405 410 415

Asn Pro Pro Phe
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<213> Acremonium sp.T178-4 NP001132

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Tyr Ala Ser Val Tyr Ser Asp Ala Gly Ser Pro Ala Ala Leu Arg Gly
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ctc gct acc aac gtc gcc aat tac aac gcc tgg aca atc gat acc tgc 96
Leu Ala Thr Asn Val Ala Asn Tyr Asn Ala Trp Thr Ile Asp Thr Cys
20 25 30
cct tca tac aca cag ggt aac tcc att tgc gac gag aag gac tac atc 144
Pro Ser Tyr Thr Gln Gly Asn Ser Ile Cys Asp Glu Lys Asp Tyr Ile
35 40 45
aat gcg ctt gct ccc ctg ctt cgc agc tca ggg ctt acg gac gct cat 192
Asn Ala Leu Ala Pro Leu Leu Arg Ser Ser Gly Leu Thr Asp Ala His
50 55 60
ttc atc act gat acc ggc cgc aac ggc aag caa cca aca ggc caa caa 240
Phe Ile Thr Asp Thr Gly Arg Asn Gly Lys Gln Pro Thr Gly Gln Gln
65 70 75 80
gcc tgg ggc gac tgg tgc aat gtc atc ggc acg ggc ttt ggc gtg cgc 288
Ala Trp Gly Asp Trp Cys Asn Val Ile Gly Thr Gly Phe Gly Val Arg
85 90 95
ccg tcc acg aac aca ggt gat tct tta ctt gac gcc ttc gtc tgg gtt 336
Pro Ser Thr Asn Thr Gly Asp Ser Leu Leu Asp Ala Phe Val Trp Val
100 105 110
aaa ccc ggt ggc gag agt gac ggg act tct gat act tgt gcg gcg cgg 384
Lys Pro Gly Gly Glu Ser Asp Gly Thr Ser Asp Thr Cys Ala Ala Arg
115 120 125
tat gat gcg cat tgc ggg tat agc gat gcg ctg ca 419
Tyr Asp Ala His Cys Gly Tyr Ser Asp Ala Leu
130 135

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 <212> PRT
 <213> Acremonium sp.T178-4 NP001132

<400> 6

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Leu Ala Thr Asn Val Ala Asn Tyr Asn Ala Trp Thr Ile Asp Thr Cys
 20 25 30

Pro Ser Tyr Thr Gln Gly Asn Ser Ile Cys Asp Glu Lys Asp Tyr Ile
 35 40 45

Asn Ala Leu Ala Pro Leu Leu Arg Ser Ser Gly Leu Thr Asp Ala His
 50 55 60

Phe Ile Thr Asp Thr Gly Arg Asn Gly Lys Gln Pro Thr Gly Gln Gln
 65 70 75 80

Ala Trp Gly Asp Trp Cys Asn Val Ile Gly Thr Gly Phe Gly Val Arg
 85 90 95

Pro Ser Thr Asn Thr Gly Asp Ser Leu Leu Asp Ala Phe Val Trp Val
 100 105 110

Lys Pro Gly Gly Glu Ser Asp Gly Thr Ser Asp Thr Cys Ala Ala Arg
 115 120 125

Tyr Asp Ala His Cys Gly Tyr Ser Asp Ala Leu
 130 135

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 <211> 306
 <212> DNA
 <213> Melanocarpus sp. AT181-3 NP001133

<220>
 <221> CDS
 <222> (1)..(306)

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48

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aac	tac	aat	gcc	tgg	agc	gtc	gcc	tcg	gcc	ccg	cct	tac	acc	agc	ccc		96
Asn	Tyr	Asn	Ala	Trp	Ser	Val	Ala	Ser	Ala	Pro	Pro	Tyr	Thr	Ser	Pro		
			20					25					30				
aac	ccc	aac	tac	gat	gag	aag	cac	tac	att	gag	gcc	ttc	agc	cct	ctc		144
Asn	Pro	Asn	Tyr	Asp	Glu	Lys	His	Tyr	Ile	Glu	Ala	Phe	Ser	Pro	Leu		
			35				40					45					
ctt	gag	gcc	cgc	ggc	ttc	cct	gcc	cgc	ttc	atc	gtc	gac	cag	ggc	cgc		192
Leu	Glu	Ala	Arg	Gly	Phe	Pro	Ala	Arg	Phe	Ile	Val	Asp	Gln	Gly	Arg		
	50					55					60						
agc	ggc	aag	cag	ccc	acc	ggc	cag	aag	gag	tgg	ggc	cac	tgg	tgc	aac		240
Ser	Gly	Lys	Gln	Pro	Thr	Gly	Gln	Lys	Glu	Trp	Gly	His	Trp	Cys	Asn		
					70				75						80		
gct	atc	ggc	acc	ggc	ttc	ggc	att	cgc	ccg	acc	gcc	aac	acc	ggc	cac		288
Ala	Ile	Gly	Thr	Gly	Phe	Gly	Ile	Arg	Pro	Thr	Ala	Asn	Thr	Gly	His		
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aac	ctg	gtt	gat	gcc	ttc												306
Asn	Leu	Val	Asp	Ala	Phe												
				100													

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Asn	Tyr	Asn	Ala	Trp	Ser	Val	Ala	Ser	Ala	Pro	Pro	Tyr	Thr	Ser	Pro		
			20					25					30				
Asn	Pro	Asn	Tyr	Asp	Glu	Lys	His	Tyr	Ile	Glu	Ala	Phe	Ser	Pro	Leu		
			35				40					45					
Leu	Glu	Ala	Arg	Gly	Phe	Pro	Ala	Arg	Phe	Ile	Val	Asp	Gln	Gly	Arg		
	50					55					60						
Ser	Gly	Lys	Gln	Pro	Thr	Gly	Gln	Lys	Glu	Trp	Gly	His	Trp	Cys	Asn		
					70				75						80		
Ala	Ile	Gly	Thr	Gly	Phe	Gly	Ile	Arg	Pro	Thr	Ala	Asn	Thr	Gly	His		
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Asn Leu Val Asp Ala Phe
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<211> 432
<212> DNA
<213> Thielavia cf. microspora T046-1 NP001134

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<222> (1)..(432)

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Ala Asn Ile Gln Pro Ala Ala Thr Leu Phe Ala Gly Ile Tyr Ser Asp
1 5 10 15
gct ggc aag ccc gcc tcg gtc cgc ggt ttg gcc acc aac gtg gcc aac 96
Ala Gly Lys Pro Ala Ser Val Arg Gly Leu Ala Thr Asn Val Ala Asn
20 25 30
tac aac gcc tgg agc ctg tcg tcg gcg ccg tcg tac acg agc ccc aac 144
Tyr Asn Ala Trp Ser Leu Ser Ser Ala Pro Ser Tyr Thr Ser Pro Asn
35 40 45
gcc aac tac gac gag aag cac tac gtc gag gcc ttt gcc ccg ctc ctc 192
Ala Asn Tyr Asp Glu Lys His Tyr Val Glu Ala Phe Ala Pro Leu Leu
50 55 60
cag gcg gcc ggc ttc ccc gcc aag ttc atc acc gac acg ggc cgc aac 240
Gln Ala Ala Gly Phe Pro Ala Lys Phe Ile Thr Asp Thr Gly Arg Asn
65 70 75 80
ggc aag cag ccc acg ggc cag agc gcg tgg ggc gac tgg tgc aac gtc 288
Gly Lys Gln Pro Thr Gly Gln Ser Ala Trp Gly Asp Trp Cys Asn Val
85 90 95
aag ggc acc ggc ttc ggt gtc cgc ccg acc tcg gag acg ggc cac gac 336
Lys Gly Thr Gly Phe Gly Val Arg Pro Thr Ser Glu Thr Gly His Asp
100 105 110
ctc ctc gac gcc ttc gtc tgg gtc aag ccc ggt ggc gag tcg gac ggc 384
Leu Leu Asp Ala Phe Val Trp Val Lys Pro Gly Gly Glu Ser Asp Gly
115 120 125
acc agc gac acc agc gcc gcc cgc tac gac tac cac tgc ggt ctg tcg 432
Thr Ser Asp Thr Ser Ala Ala Arg Tyr Asp Tyr His Cys Gly Leu Ser
130 135 140

<210> 10
<211> 144
<212> PRT

<213> Thielavia cf. microspora T046-1 NP001134

<400> 10

Ala Asn Ile Gln Pro Ala Ala Thr Leu Phe Ala Gly Ile Tyr Ser Asp
1 5 10 15

Ala Gly Lys Pro Ala Ser Val Arg Gly Leu Ala Thr Asn Val Ala Asn
20 25 30

Tyr Asn Ala Trp Ser Leu Ser Ser Ala Pro Ser Tyr Thr Ser Pro Asn
35 40 45

Ala Asn Tyr Asp Glu Lys His Tyr Val Glu Ala Phe Ala Pro Leu Leu
50 55 60

Gln Ala Ala Gly Phe Pro Ala Lys Phe Ile Thr Asp Thr Gly Arg Asn
65 70 75 80

Gly Lys Gln Pro Thr Gly Gln Ser Ala Trp Gly Asp Trp Cys Asn Val
85 90 95

Lys Gly Thr Gly Phe Gly Val Arg Pro Thr Ser Glu Thr Gly His Asp
100 105 110

Leu Leu Asp Ala Phe Val Trp Val Lys Pro Gly Gly Glu Ser Asp Gly
115 120 125

Thr Ser Asp Thr Ser Ala Ala Arg Tyr Asp Tyr His Cys Gly Leu Ser
130 135 140

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<212> DNA

<213> Aspergillus sp. T186-2 NP001136

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Gly Leu Phe Gly Trp Pro Ala Asn Leu Thr Pro Ser Ala Arg Leu Phe
1 5 10 15

gcc caa atc tac aag gat gcc ggc agg tct gcc ttc atc cgt ggt ctt 96
Ala Gln Ile Tyr Lys Asp Ala Gly Arg Ser Ala Phe Ile Arg Gly Leu

	20	25	30	
gcc acc aac gtc tcc aac tac aac gcc ctc agt gca acc acc cgt gat				144
Ala Thr Asn Val Ser Asn Tyr Asn Ala Leu Ser Ala Thr Thr Arg Asp				
	35	40	45	
ccc gtc acc cag ggc aat gac aac tac gat gag ctc cgc ttc atc aac				192
Pro Val Thr Gln Gly Asn Asp Asn Tyr Asp Glu Leu Arg Phe Ile Asn				
	50	55	60	
gct ctt gct cct ctc ctc cga aat gaa ggc tgg gac gcc aag ttc atc				240
Ala Leu Ala Pro Leu Leu Arg Asn Glu Gly Trp Asp Ala Lys Phe Ile				
	65	70	75	80
gtc gac cag ggt cgt tct ggt gtc cag aac atc cga cag gag tgg ggc				288
Val Asp Gln Gly Arg Ser Gly Val Gln Asn Ile Arg Gln Glu Trp Gly				
	85	90	95	
gac tgg tgc				297
Asp Trp Cys				

<210> 12
 <211> 99
 <212> PRT
 <213> Aspergillus sp. T186-2 NP001136

<400> 12

Gly Leu Phe Gly Trp Pro Ala Asn Leu Thr Pro Ser Ala Arg Leu Phe
1 5 10 15

Ala Gln Ile Tyr Lys Asp Ala Gly Arg Ser Ala Phe Ile Arg Gly Leu
20 25 30

Ala Thr Asn Val Ser Asn Tyr Asn Ala Leu Ser Ala Thr Thr Arg Asp
35 40 45

Pro Val Thr Gln Gly Asn Asp Asn Tyr Asp Glu Leu Arg Phe Ile Asn
50 55 60

Ala Leu Ala Pro Leu Leu Arg Asn Glu Gly Trp Asp Ala Lys Phe Ile
65 70 75 80

Val Asp Gln Gly Arg Ser Gly Val Gln Asn Ile Arg Gln Glu Trp Gly
85 90 95

Asp Trp Cys

<210> 13
 <211> 420
 <212> DNA
 <213> Thielavia cf. australiensis T55-15 NP001000

<220>
 <221> CDS
 <222> (1)..(420)

<400> 13
 tgg ctg ggg tgg ccc gcc aac atc cag ccc gct gct acc ctg ttc gcc 48
 Trp Leu Gly Trp Pro Ala Asn Ile Gln Pro Ala Ala Thr Leu Phe Ala
 1 5 10 15
 ggc atc tac aac gac gct ggc aag ccc gcc tcg gtc cgt ggt ctg gcc 96
 Gly Ile Tyr Asn Asp Ala Gly Lys Pro Ala Ser Val Arg Gly Leu Ala
 20 25 30
 acc aac gtt gcc aac tac aac gcc tgg agc ctg tcc tcg gcc ccg tcg 144
 Thr Asn Val Ala Asn Tyr Asn Ala Trp Ser Leu Ser Ser Ala Pro Ser
 35 40 45
 tac acg acc ccc aac gcc aac tac gac gag aag cac tac gtc gag gcc 192
 Tyr Thr Thr Pro Asn Ala Asn Tyr Asp Glu Lys His Tyr Val Glu Ala
 50 55 60
 ttt gcc ccg ctt ctc tcg gcc gct ggc ttc ccc gcc aag ttc atc acc 240
 Phe Ala Pro Leu Leu Ser Ala Ala Gly Phe Pro Ala Lys Phe Ile Thr
 65 70 75 80
 gac act ggc cgc aac ggc aag cag ccc acc ggc cag agc cag tgg ggc 288
 Asp Thr Gly Arg Asn Gly Lys Gln Pro Thr Gly Gln Ser Gln Trp Gly
 85 90 95
 gat tgg tgc aac gtc aag ggc acc ggc ttc ggt gtc cgc ccg acc tcc 336
 Asp Trp Cys Asn Val Lys Gly Thr Gly Phe Gly Val Arg Pro Thr Ser
 100 105 110
 gag acg ggc cac gag ctc ctg gat gcc ttt gtc tgg gcc aag ccc ggt 384
 Glu Thr Gly His Glu Leu Leu Asp Ala Phe Val Trp Ala Lys Pro Gly
 115 120 125
 ggc gag tcc gac ggt acc agc gac acc agc gct gcc 420
 Gly Glu Ser Asp Gly Thr Ser Asp Thr Ser Ala Ala
 130 135 140

<210> 14
 <211> 140
 <212> PRT
 <213> Thielavia cf. australiensis T55-15 NP001000

<400> 14

Trp Leu Gly Trp Pro Ala Asn Ile Gln Pro Ala Ala Thr Leu Phe Ala

1	5	10	15
Gly Ile Tyr Asn Asp Ala Gly Lys Pro Ala Ser Val Arg Gly Leu Ala	20	25	30
Thr Asn Val Ala Asn Tyr Asn Ala Trp Ser Leu Ser Ser Ala Pro Ser	35	40	45
Tyr Thr Thr Pro Asn Ala Asn Tyr Asp Glu Lys His Tyr Val Glu Ala	50	55	60
Phe Ala Pro Leu Leu Ser Ala Ala Gly Phe Pro Ala Lys Phe Ile Thr	65	70	75
Asp Thr Gly Arg Asn Gly Lys Gln Pro Thr Gly Gln Ser Gln Trp Gly	85	90	95
Asp Trp Cys Asn Val Lys Gly Thr Gly Phe Gly Val Arg Pro Thr Ser	100	105	110
Glu Thr Gly His Glu Leu Leu Asp Ala Phe Val Trp Ala Lys Pro Gly	115	120	125
Gly Glu Ser Asp Gly Thr Ser Asp Thr Ser Ala Ala	130	135	140

<210> 15
 <211> 1221
 <212> DNA
 <213> Aspergillus tubingensis NP001143

<220>
 <221> CDS
 <222> (1)..(1221)

<220>
 <221> misc_feature
 <222> (903)..(903)
 <223> n is a, c, g, or t

<220>
 <221> misc_feature
 <222> (1011)..(1011)
 <223> n is a, c, g, or t

<220>
 <221> misc_feature

<222> (1017)..(1017)

<223> n is a, c, g, or t

<400> 15

atg	aat	atg	cac	tcc	atc	aac	atg	cga	gcc	atc	tgg	ccc	ctc	gtc	tct	48
Met	Asn	Met	His	Ser	Ile	Asn	Met	Arg	Ala	Ile	Trp	Pro	Leu	Val	Ser	
1				5					10					15		

ctc	ttc	tct	gcc	gtt	aag	gcc	ctc	ccc	gcc	gca	agc	gcg	act	gct	tca	96
Leu	Phe	Ser	Ala	Val	Lys	Ala	Leu	Pro	Ala	Ala	Ser	Ala	Thr	Ala	Ser	
			20					25					30			

gcg	tct	gtt	gcg	gcc	tcg	agc	tct	ccg	gcg	ccg	act	gcc	tct	gct	acc	144
Ala	Ser	Val	Ala	Ala	Ser	Ser	Ser	Pro	Ala	Pro	Thr	Ala	Ser	Ala	Thr	
		35					40					45				

ggc	aat	ccc	ttt	gag	gga	tac	cag	ctc	tat	gtg	aac	ccc	tac	tat	aag	192
Gly	Asn	Pro	Phe	Glu	Gly	Tyr	Gln	Leu	Tyr	Val	Asn	Pro	Tyr	Tyr	Lys	
	50					55					60					

tcg	caa	gtg	gag	agt	tcg	gcc	att	cca	tca	ttg	tct	gct	agt	tcg	ctg	240
Ser	Gln	Val	Glu	Ser	Ser	Ala	Ile	Pro	Ser	Leu	Ser	Ala	Ser	Ser	Leu	
65					70					75					80	

gtc	gcg	cag	gcg	agt	gct	gca	gcc	gat	gtg	cct	tca	ttt	tac	tgg	cta	288
Val	Ala	Gln	Ala	Ser	Ala	Ala	Ala	Asp	Val	Pro	Ser	Phe	Tyr	Trp	Leu	
				85					90					95		

gac	acg	gcc	gac	aag	gtg	cct	acc	atg	ggc	gaa	tat	ctg	gat	gac	atc	336
Asp	Thr	Ala	Asp	Lys	Val	Pro	Thr	Met	Gly	Glu	Tyr	Leu	Asp	Asp	Ile	
			100					105					110			

cag	acg	caa	aac	gcc	gct	gga	gcg	aat	cct	ccc	att	gct	ggc	atc	ttc	384
Gln	Thr	Gln	Asn	Ala	Ala	Gly	Ala	Asn	Pro	Pro	Ile	Ala	Gly	Ile	Phe	
		115					120					125				

gtc	gtc	tat	gac	ctg	ccg	gat	ccg	gat	tgc	gct	gcc	ttg	gct	agt	aat	432
Val	Val	Tyr	Asp	Leu	Pro	Asp	Arg	Asp	Cys	Ala	Ala	Leu	Ala	Ser	Asn	
	130					135					140					

ggg	gaa	tac	gcg	atc	agt	gat	gga	ggc	gtg	gag	aag	tat	aag	gcg	tac	480
Gly	Glu	Tyr	Ala	Ile	Ser	Asp	Gly	Gly	Val	Glu	Lys	Tyr	Lys	Ala	Tyr	
145					150				155					160		

att	gat	tct	att	cgc	gag	cag	gtc	gag	acg	tac	tcg	gat	gtt	cag	act	528
Ile	Asp	Ser	Ile	Arg	Glu	Gln	Val	Glu	Thr	Tyr	Ser	Asp	Val	Gln	Thr	
				165					170					175		

att	ttg	att	atc	gaa	ccg	gat	agc	tta	gct	aac	ctg	gtg	acg	aat	ctc	576
Ile	Leu	Ile	Ile	Glu	Pro	Asp	Ser	Leu	Ala	Asn	Leu	Val	Thr	Asn	Leu	
			180					185					190			

gat	gtg	gct	aaa	tgc	gcc	aat	gct	caa	tct	gct	tac	ctg	gaa	tgc	acc	624
Asp	Val	Ala	Lys	Cys	Ala	Asn	Ala	Gln	Ser	Ala	Tyr	Leu	Glu	Cys	Thr	
		195					200					205				

aat	tat	gca	ctt	gag	cag	ttg	aat	ctr	ccg	aac	gtg	gct	atg	tat	ctt	672
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

Asn Tyr Ala Leu Glu Gln Leu Asn Xaa Pro Asn Val Ala Met Tyr Leu	
210 215 220	
gat gct ggc cat gct gga tgg ctg gga tgg cct gcc aac atc ggt ccc	720
Asp Ala Gly His Ala Gly Trp Leu Gly Trp Pro Ala Asn Ile Gly Pro	
225 230 235 240	
gcg gcg gaa ctc tac gca tcg gtg tat aag aat gcg tcg tct cca gca	768
Ala Ala Glu Leu Tyr Ala Ser Val Tyr Lys Asn Ala Ser Ser Pro Ala	
245 250 255	
gct gtt cgt gga ctc gct aca rac gta gct aac ttc aat gcc tgg agc	816
Ala Val Arg Gly Leu Ala Thr Xaa Val Ala Asn Phe Asn Ala Trp Ser	
260 265 270	
atc gac act tgc ccc tcc tat acw tcg ggt aac gat gtc tgt gat gaa	864
Ile Asp Thr Cys Pro Ser Tyr Xaa Ser Gly Asn Asp Val Cys Asp Glu	
275 280 285	
aaa agc tac atc aat gcc ttt gca ccg gag ctc tct agn gct gga ttt	912
Lys Ser Tyr Ile Asn Ala Phe Ala Pro Glu Leu Ser Xaa Ala Gly Phe	
290 295 300	
gat gcc cac ttt att acc gat acg ggt cgc aat gga aag cag cct act	960
Asp Ala His Phe Ile Thr Asp Thr Gly Arg Asn Gly Lys Gln Pro Thr	
305 310 315 320	
gga caa agc gcg tgg ggt gac tgg ggc aat gtc aag gat act ggc ttc	1008
Gly Gln Ser Ala Trp Gly Asp Trp Gly Asn Val Lys Asp Thr Gly Phe	
325 330 335	
ggn gct can ccg aca acc gat act gga aac gag ctg gct gat gcc ttt	1056
Gly Ala Xaa Pro Thr Thr Asp Thr Gly Asn Glu Leu Ala Asp Ala Phe	
340 345 350	
gtc tgg gyc aac cct ggc gga aag agt gat ggg acg tcg gac act agc	1104
Val Trp Xaa Asn Pro Gly Gly Lys Ser Asp Gly Thr Ser Asp Thr Ser	
355 360 365	
tct tct cgc tac gat gcg cat tgc gga tat agt gat gct ttg cag cct	1152
Ser Ser Arg Tyr Asp Ala His Cys Gly Tyr Ser Asp Ala Leu Gln Pro	
370 375 380	
gcc ccg gag gct ggt act tgg ttc cag gca tac ttt gag cag ctt ttg	1200
Ala Pro Glu Ala Gly Thr Trp Phe Gln Ala Tyr Phe Glu Gln Leu Leu	
385 390 395 400	
acc aat gcc aac cct tcc ctg	1221
Thr Asn Ala Asn Pro Ser Leu	
405	

<210> 16
 <211> 407
 <212> PRT
 <213> Aspergillus tubingensis NP001143

<220>
 <221> misc_feature
 <222> (217)..(217)
 <223> The 'Xaa' at location 217 stands for Leu.

<220>
 <221> misc_feature
 <222> (264)..(264)
 <223> The 'Xaa' at location 264 stands for Asp, or Asn.

<220>
 <221> misc_feature
 <222> (280)..(280)
 <223> The 'Xaa' at location 280 stands for Thr.

<220>
 <221> misc_feature
 <222> (301)..(301)
 <223> The 'Xaa' at location 301 stands for Arg, or Ser.

<220>
 <221> misc_feature
 <222> (339)..(339)
 <223> The 'Xaa' at location 339 stands for Gln, or His.

<220>
 <221> misc_feature
 <222> (355)..(355)
 <223> The 'Xaa' at location 355 stands for Ala, or Val.

<400> 16

Met	Asn	Met	His	Ser	Ile	Asn	Met	Arg	Ala	Ile	Trp	Pro	Leu	Val	Ser
1				5					10					15	
Leu	Phe	Ser	Ala	Val	Lys	Ala	Leu	Pro	Ala	Ala	Ser	Ala	Thr	Ala	Ser
			20					25					30		
Ala	Ser	Val	Ala	Ala	Ser	Ser	Ser	Pro	Ala	Pro	Thr	Ala	Ser	Ala	Thr
		35					40					45			
Gly	Asn	Pro	Phe	Glu	Gly	Tyr	Gln	Leu	Tyr	Val	Asn	Pro	Tyr	Tyr	Lys
	50					55					60				
Ser	Gln	Val	Glu	Ser	Ser	Ala	Ile	Pro	Ser	Leu	Ser	Ala	Ser	Ser	Leu
65					70					75					80
Val	Ala	Gln	Ala	Ser	Ala	Ala	Ala	Asp	Val	Pro	Ser	Phe	Tyr	Trp	Leu
				85					90					95	
Asp	Thr	Ala	Asp	Lys	Val	Pro	Thr	Met	Gly	Glu	Tyr	Leu	Asp	Asp	Ile

Gly Ala Xaa Pro Thr Thr Asp Thr Gly Asn Glu Leu Ala Asp Ala Phe
 340 345 350

Val Trp Xaa Asn Pro Gly Gly Lys Ser Asp Gly Thr Ser Asp Thr Ser
 355 360 365

Ser Ser Arg Tyr Asp Ala His Cys Gly Tyr Ser Asp Ala Leu Gln Pro
 370 375 380

Ala Pro Glu Ala Gly Thr Trp Phe Gln Ala Tyr Phe Glu Gln Leu Leu
 385 390 395 400

Thr Asn Ala Asn Pro Ser Leu
 405

<210> 17
 <211> 429
 <212> DNA
 <213> Gloeophyllum trabeum NP001144

<220>
 <221> CDS
 <222> (1)..(429)

<400> 17
 gca tcg tct cca gca gct gtt cgt gga ctc gct aca aac gta gct aac 48
 Ala Ser Ser Pro Ala Ala Val Arg Gly Leu Ala Thr Asn Val Ala Asn
 1 5 10 15
 ttc aat gcc tgg agc atc gac act tgc ccc tcc tat aca tcg ggt aac 96
 Phe Asn Ala Trp Ser Ile Asp Thr Cys Pro Ser Tyr Thr Ser Gly Asn
 20 25 30
 gat gtc tgt gat gag aag agc tac atc aat gcc ttt gca ccg gag ctc 144
 Asp Val Cys Asp Glu Lys Ser Tyr Ile Asn Ala Phe Ala Pro Glu Leu
 35 40 45
 tct agt gct gga ttt gat gcc cac ttt att acc gat acg ggt cgc aat 192
 Ser Ser Ala Gly Phe Asp Ala His Phe Ile Thr Asp Thr Gly Arg Asn
 50 55 60
 gga aag cag cct act gga cag agc gcg tgg ggt gac tgg tgc aat gtc 240
 Gly Lys Gln Pro Thr Gly Gln Ser Ala Trp Gly Asp Trp Cys Asn Val
 65 70 75 80
 aag gat act ggc ttc ggt gct cag ccg acg acc gat act gga gac gag 288
 Lys Asp Thr Gly Phe Gly Ala Gln Pro Thr Thr Asp Thr Gly Asp Glu
 85 90 95

ctg gct gat gcc ttt gtc tgg gtc aag cct ggc gga gag agt gat ggg	336
Leu Ala Asp Ala Phe Val Trp Val Lys Pro Gly Gly Glu Ser Asp Gly	
100 105 110	

acg tcg gac act agc tct tct cgc tac gat gcg cat tgc gga tat agt	384
Thr Ser Asp Thr Ser Ser Ser Arg Tyr Asp Ala His Cys Gly Tyr Ser	
115 120 125	

gat gct ttg cag cct gcc ccg gag gct ggt act tgg ttc caa ggc	429
Asp Ala Leu Gln Pro Ala Pro Glu Ala Gly Thr Trp Phe Gln Gly	
130 135 140	

<210> 18
 <211> 143
 <212> PRT
 <213> Gloeophyllum trabeum NP001144

<400> 18

Ala Ser Ser Pro Ala Ala Val Arg Gly Leu Ala Thr Asn Val Ala Asn
1 5 10 15

Phe Asn Ala Trp Ser Ile Asp Thr Cys Pro Ser Tyr Thr Ser Gly Asn
20 25 30

Asp Val Cys Asp Glu Lys Ser Tyr Ile Asn Ala Phe Ala Pro Glu Leu
35 40 45

Ser Ser Ala Gly Phe Asp Ala His Phe Ile Thr Asp Thr Gly Arg Asn
50 55 60

Gly Lys Gln Pro Thr Gly Gln Ser Ala Trp Gly Asp Trp Cys Asn Val
65 70 75 80

Lys Asp Thr Gly Phe Gly Ala Gln Pro Thr Thr Asp Thr Gly Asp Glu
85 90 95

Leu Ala Asp Ala Phe Val Trp Val Lys Pro Gly Gly Glu Ser Asp Gly
100 105 110

Thr Ser Asp Thr Ser Ser Ser Arg Tyr Asp Ala His Cys Gly Tyr Ser
115 120 125

Asp Ala Leu Gln Pro Ala Pro Glu Ala Gly Thr Trp Phe Gln Gly
130 135 140

<210> 19

<211> 213
 <212> DNA
 <213> Meripilus giganteus ND001631

<220>
 <221> misc_feature
 <222> (1)..(213)
 <223> y is c or t

<400> 19
 aaactcggag tacgtctgga acaagtgccg gcctcnggcr gctgggtacc gtcttcgtcc 60
 gacagacagc asgtgctgtc gtaccggtrg cgacgagctg ttcgaggtay cgtcggactc 120
 ryctccgggm ttcaccaga tkatcacgtc tatgasyygg ttgcccggtg tcgtcctcat 180
 ggcgcgtgcc gaagccgttg cccttgatgt tgc 213

<210> 20
 <211> 71
 <212> PRT
 <213> Meripilus giganteus ND001631 enzyme

<220>
 <221> MISC_FEATURE
 <222> (1)..(71)
 <223> x is any amino acid

<400> 20

Ala	Thr	Ser	Arg	Ala	Thr	Ala	Ser	Ala	Arg	Ala	Met	Arg	Thr	Asn	Thr
1				5					10					15	
Gly	Asn	Pro	Xaa	Ile	Asp	Val	Ile	Ile	Trp	Val	Xaa	Pro	Gly	Xaa	Glu
			20					25					30		
Ser	Asp	Xaa	Thr	Ser	Asn	Ser	Ser	Ser	Xaa	Pro	Val	Arg	Gln	His	Xaa
		35					40					45			
Leu	Ser	Val	Gly	Arg	Arg	Arg	Tyr	Pro	Ala	Ala	Xaa	Gly	Arg	His	Leu
	50					55					60				
Phe	Gln	Thr	Tyr	Ser	Glu	Phe									
65					70										

<210> 21
 <211> 782
 <212> DNA
 <213> Trichophaea saccata NP000960

<220>

<221> CDS

<222> (43)..(702)

<400> 21

ggcacgaggg cagatcgatc gactcgagga ccacatcgca tc atg aag aac ttc 54
Met Lys Asn Phe
1

ctt ctg gcg tcc gcg ctg atc gcg gtt gcc gca gct cag cag agt gct 102
Leu Leu Ala Ser Ala Leu Ile Ala Val Ala Ala Ala Gln Gln Ser Ala
5 10 15 20

tgg gga cag tgc ggt gga att ggc tgg act ggc gcg acg act tgt atc 150
Trp Gly Gln Cys Gly Gly Ile Gly Trp Thr Gly Ala Thr Thr Cys Ile
25 30 35

tct ggc tac acg tgc tca aag atc aac gac tac tat tcc cag tgc att 198
Ser Gly Tyr Thr Cys Ser Lys Ile Asn Asp Tyr Tyr Ser Gln Cys Ile
40 45 50

ccg ggt acg gct tca acc acc act caa ggc ggc ggc aat ggc gga gga 246
Pro Gly Thr Ala Ser Thr Thr Thr Gln Gly Gly Gly Asn Gly Gly Gly
55 60 65

aac ggc ggt aca acg act act ccc act acc act cca gcg gcc agt aac 294
Asn Gly Gly Thr Thr Thr Thr Pro Thr Thr Thr Pro Ala Ala Ser Asn
70 75 80

acc aac aac ccg ttc tcc ggc aag acc caa tgg gcg aac cct tac tac 342
Thr Asn Asn Pro Phe Ser Gly Lys Thr Gln Trp Ala Asn Pro Tyr Tyr
85 90 95 100

gct tcc gag gtc tcg agc atc gcc atc ccg tcc ctc gtt gcc gcc gga 390
Ala Ser Glu Val Ser Ser Ile Ala Ile Pro Ser Leu Val Ala Ala Gly
105 110 115

aac acc cac tac atc gtc gac caa ggc cgc agc ggc aag cag ccg acc 438
Asn Thr His Tyr Ile Val Asp Gln Gly Arg Ser Gly Lys Gln Pro Thr
120 125 130

ggc cag ctc cag cag ggc gat tgg tgc aac gcc ctg gga acc ggc ttt 486
Gly Gln Leu Gln Gln Gly Asp Trp Cys Asn Ala Leu Gly Thr Gly Phe
135 140 145

gga att cgt cct gat aca acc ccg gat gat ccc aac ctt gat gct ttc 534
Gly Ile Arg Pro Asp Thr Thr Pro Asp Asp Pro Asn Leu Asp Ala Phe
150 155 160

gtg tgg gtt aag ccg ggt ggt gaa tcg gat ggt acc agc aat act tcc 582
Val Trp Val Lys Pro Gly Gly Glu Ser Asp Gly Thr Ser Asn Thr Ser
165 170 175 180

tcg acc cgc tat gat tat cat tgt gga cag agc gat gcg cta caa ccg 630
Ser Thr Arg Tyr Asp Tyr His Cys Gly Gln Ser Asp Ala Leu Gln Pro

	185	190	195	
gcc ccg gag gcg gga acg tgg ttc cag gcg tat ttt gtg cag ttg ctg				678
Ala Pro Glu Ala Gly Thr Trp Phe Gln Ala Tyr Phe Val Gln Leu Leu				
	200	205	210	
cag aat gct aat cct agc ttc acg taagcttggg agcgtggggg ttggaagatg				732
Gln Asn Ala Asn Pro Ser Phe Thr				
	215	220		
tgtattgtat gtgtagatag agaaaaactg ttggcctatt caggactaag				782
<210>	22			
<211>	220			
<212>	PRT			
<213>	Trichophaea saccata NP000960			
<400>	22			
Met Lys Asn Phe Leu Leu Ala Ser Ala Leu Ile Ala Val Ala Ala Ala				
1	5	10	15	
Gln Gln Ser Ala Trp Gly Gln Cys Gly Gly Ile Gly Trp Thr Gly Ala				
	20	25	30	
Thr Thr Cys Ile Ser Gly Tyr Thr Cys Ser Lys Ile Asn Asp Tyr Tyr				
	35	40	45	
Ser Gln Cys Ile Pro Gly Thr Ala Ser Thr Thr Thr Gln Gly Gly Gly				
	50	55	60	
Asn Gly Gly Gly Asn Gly Gly Thr Thr Thr Thr Pro Thr Thr Thr Pro				
65	70	75	80	
Ala Ala Ser Asn Thr Asn Asn Pro Phe Ser Gly Lys Thr Gln Trp Ala				
	85	90	95	
Asn Pro Tyr Tyr Ala Ser Glu Val Ser Ser Ile Ala Ile Pro Ser Leu				
	100	105	110	
Val Ala Ala Gly Asn Thr His Tyr Ile Val Asp Gln Gly Arg Ser Gly				
	115	120	125	
Lys Gln Pro Thr Gly Gln Leu Gln Gln Gly Asp Trp Cys Asn Ala Leu				
	130	135	140	
Gly Thr Gly Phe Gly Ile Arg Pro Asp Thr Thr Pro Asp Asp Pro Asn				

145		150		155		160
Leu Asp Ala Phe Val Trp Val Lys Pro Gly Gly Glu Ser Asp Gly Thr						
	165			170		175
Ser Asn Thr Ser Ser Thr Arg Tyr Asp Tyr His Cys Gly Gln Ser Asp						
	180			185		190
Ala Leu Gln Pro Ala Pro Glu Ala Gly Thr Trp Phe Gln Ala Tyr Phe						
	195			200		205
Val Gln Leu Leu Gln Asn Ala Asn Pro Ser Phe Thr						
	210			215		220

<210> 23
 <211> 1587
 <212> DNA
 <213> Stibella annulata NP001040

<220>
 <221> CDS
 <222> (21)..(1394)

<400> 23	
ggcacgaggc gcgcatacaca atg gcc ggt cga ttc ttc ctc tct gct gcc ttc	53
Met Ala Gly Arg Phe Phe Leu Ser Ala Ala Phe	
1 5 10	
ctg gct agc gcg gct ttg gcc gtc cct ctc gag gag agg cag aac tgc	101
Leu Ala Ser Ala Ala Leu Ala Val Pro Leu Glu Glu Arg Gln Asn Cys	
15 20 25	
tcc ccg cag tgg gcc cag tgc ggt gga aat gga tgg agc ggt ccg acg	149
Ser Pro Gln Trp Ala Gln Cys Gly Gly Asn Gly Trp Ser Gly Pro Thr	
30 35 40	
tgc tgc gcc tcc ggc agc aac tgc cag gtc acc aac gag tgg tac tct	197
Cys Cys Ala Ser Gly Ser Asn Cys Gln Val Thr Asn Glu Trp Tyr Ser	
45 50 55	
cag tgt gtt ccg ggc gcg gcg cct ccc cct ccc ccc gtc acc acg acg	245
Gln Cys Val Pro Gly Ala Ala Pro Pro Pro Pro Pro Val Thr Thr Thr	
60 65 70 75	
cgg tcg acc acc acg ccc ccg acg acg acg acc agg acc acc gct gat	293
Arg Ser Thr Thr Thr Pro Pro Thr Thr Thr Thr Arg Thr Thr Ala Asp	
80 85 90	
gcc cct cct ccc acc ggc ggc gct act tac acc ggc aac ccc ttc ctc	341
Ala Pro Pro Pro Thr Gly Gly Ala Thr Tyr Thr Gly Asn Pro Phe Leu	
95 100 105	

ggt gtc aac cag tgg gcc aac aac ttc tac cgg tct gag atc atg aac Gly Val Asn Gln Trp Ala Asn Asn Phe Tyr Arg Ser Glu Ile Met Asn 110 115 120	389
atc gcc gtc ccg tcc ctg tcc ggt gcc atg gct acc gcc gcc gcc aag Ile Ala Val Pro Ser Leu Ser Gly Ala Met Ala Thr Ala Ala Ala Lys 125 130 135	437
gtc gcc gat gtg ccc acc ttc cag tgg att gac aag atg gac aag ctc Val Ala Asp Val Pro Thr Phe Gln Trp Ile Asp Lys Met Asp Lys Leu 140 145 150 155	485
ccc ttg atc gat gag gct ctc gcc gac gtc cgc gct gcc aac gcc cgt Pro Leu Ile Asp Glu Ala Leu Ala Asp Val Arg Ala Ala Asn Ala Arg 160 165 170	533
ggc ggc aac tac gct tcc atc ctg gtc gtc tac aac ctg ccc gac cgt Gly Gly Asn Tyr Ala Ser Ile Leu Val Val Tyr Asn Leu Pro Asp Arg 175 180 185	581
gac tgc gcc gcc gcc gcc tcg aac ggc gag ttc gcc atc gcc gac ggc Asp Cys Ala Ala Ala Ala Ser Asn Gly Glu Phe Ala Ile Ala Asp Gly 190 195 200	629
ggt gtt gct aag tac aag aac tac att gac gag att cgc aag ctc gtc Gly Val Ala Lys Tyr Lys Asn Tyr Ile Asp Glu Ile Arg Lys Leu Val 205 210 215	677
atc aag tac aac gac ctc cgt atc atc ctg gtc atc gag ccc gac tcc Ile Lys Tyr Asn Asp Leu Arg Ile Ile Leu Val Ile Glu Pro Asp Ser 220 225 230 235	725
ctc gcc aac atg gtg acc aac atg aac gtc gcc aag tgc cag aac gcc Leu Ala Asn Met Val Thr Asn Met Asn Val Ala Lys Cys Gln Asn Ala 240 245 250	773
gcc tcg gcc tac cgg gag tgc acc aac tat gcc ctg acg aac ctc gac Ala Ser Ala Tyr Arg Glu Cys Thr Asn Tyr Ala Leu Thr Asn Leu Asp 255 260 265	821
ctg ccc aac gtc gcc cag tac atg gat gcc gga cat gct ggc tgg ctc Leu Pro Asn Val Ala Gln Tyr Met Asp Ala Gly His Ala Gly Trp Leu 270 275 280	869
ggc tgg ccc gcc aac atc acc ccc gcc gcc cag ctc ttc gcc gag gtc Gly Trp Pro Ala Asn Ile Thr Pro Ala Ala Gln Leu Phe Ala Glu Val 285 290 295	917
tac aag cag gcc ggc agc ccc aag tcg gtc cgt ggt ctg gcc atc aac Tyr Lys Gln Ala Gly Ser Pro Lys Ser Val Arg Gly Leu Ala Ile Asn 300 305 310 315	965
gtc tcc aac tac aac gcg tgg agc gtt tcg tcc cct cct ccc tac acc Val Ser Asn Tyr Asn Ala Trp Ser Val Ser Ser Pro Pro Pro Tyr Thr 320 325 330	1013

tct ccc aac ccc aac tac gac gag cgc cac ttc gtt gag gcc ttt gcg	1061
Ser Pro Asn Pro Asn Tyr Asp Glu Arg His Phe Val Glu Ala Phe Ala	
335 340 345	
ccc ctc ctg cgc cag aac ggc tgg gat gcc aag ttc atc gtc gac cag	1109
Pro Leu Leu Arg Gln Asn Gly Trp Asp Ala Lys Phe Ile Val Asp Gln	
350 355 360	
ggc cgc tcc ggc agg cag ccc acc ggc cag cag gag tgg gga cac tgg	1157
Gly Arg Ser Gly Arg Gln Pro Thr Gly Gln Gln Glu Trp Gly His Trp	
365 370 375	
tgc aac gcc atc ggc act ggc ttc ggc cag cgc ccg acg tcc aac acc	1205
Cys Asn Ala Ile Gly Thr Gly Phe Gly Gln Arg Pro Thr Ser Asn Thr	
380 385 390 395	
ggc cac gcc gat gtt gac gct ttc gtc tgg atc aag ccg ggc ggt gag	1253
Gly His Ala Asp Val Asp Ala Phe Val Trp Ile Lys Pro Gly Gly Glu	
400 405 410	
tgc gac ggc acc agc gac acc tcg gcc gcc cgc tac gac cac ttc tgt	1301
Cys Asp Gly Thr Ser Asp Thr Ser Ala Ala Arg Tyr Asp His Phe Cys	
415 420 425	
ggc aac cct gat gcc ctc aag ccg gcc ccc gaa gcc gga gag tgg ttc	1349
Gly Asn Pro Asp Ala Leu Lys Pro Ala Pro Glu Ala Gly Glu Trp Phe	
430 435 440	
cag gcc tac ttc gag cag ctt ctg cgc aac gcc aac ccc gcc ttc	1394
Gln Ala Tyr Phe Glu Gln Leu Leu Arg Asn Ala Asn Pro Ala Phe	
445 450 455	
taagtgctgg atgagctttt ctgagagggt acttccgcgg tcttgggttt cactcttctc	1454
agcctttcag ggcagcagtt ttggtttctt ggggtaggac ctccgggttt atgtagacgg	1514
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20 25 30

Gln Cys Gly Gly Asn Gly Trp Ser Gly Pro Thr Cys Cys Ala Ser Gly

35					40					45					
Ser	Asn	Cys	Gln	Val	Thr	Asn	Glu	Trp	Tyr	Ser	Gln	Cys	Val	Pro	Gly
50						55					60				
Ala	Ala	Pro	Pro	Pro	Pro	Pro	Val	Thr	Thr	Thr	Arg	Ser	Thr	Thr	Thr
65						70				75					80
Pro	Pro	Thr	Thr	Thr	Thr	Arg	Thr	Thr	Ala	Asp	Ala	Pro	Pro	Pro	Thr
				85					90					95	
Gly	Gly	Ala	Thr	Tyr	Thr	Gly	Asn	Pro	Phe	Leu	Gly	Val	Asn	Gln	Trp
			100					105					110		
Ala	Asn	Asn	Phe	Tyr	Arg	Ser	Glu	Ile	Met	Asn	Ile	Ala	Val	Pro	Ser
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Leu	Ser	Gly	Ala	Met	Ala	Thr	Ala	Ala	Ala	Lys	Val	Ala	Asp	Val	Pro
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Thr	Phe	Gln	Trp	Ile	Asp	Lys	Met	Asp	Lys	Leu	Pro	Leu	Ile	Asp	Glu
145					150					155					160
Ala	Leu	Ala	Asp	Val	Arg	Ala	Ala	Asn	Ala	Arg	Gly	Gly	Asn	Tyr	Ala
				165					170					175	
Ser	Ile	Leu	Val	Val	Tyr	Asn	Leu	Pro	Asp	Arg	Asp	Cys	Ala	Ala	Ala
			180					185					190		
Ala	Ser	Asn	Gly	Glu	Phe	Ala	Ile	Ala	Asp	Gly	Gly	Val	Ala	Lys	Tyr
		195					200					205			
Lys	Asn	Tyr	Ile	Asp	Glu	Ile	Arg	Lys	Leu	Val	Ile	Lys	Tyr	Asn	Asp
	210					215					220				
Leu	Arg	Ile	Ile	Leu	Val	Ile	Glu	Pro	Asp	Ser	Leu	Ala	Asn	Met	Val
225					230					235					240
Thr	Asn	Met	Asn	Val	Ala	Lys	Cys	Gln	Asn	Ala	Ala	Ser	Ala	Tyr	Arg
				245					250					255	
Glu	Cys	Thr	Asn	Tyr	Ala	Leu	Thr	Asn	Leu	Asp	Leu	Pro	Asn	Val	Ala
			260					265					270		

Gln Tyr Met Asp Ala Gly His Ala Gly Trp Leu Gly Trp Pro Ala Asn
 275 280 285

Ile Thr Pro Ala Ala Gln Leu Phe Ala Glu Val Tyr Lys Gln Ala Gly
 290 295 300

Ser Pro Lys Ser Val Arg Gly Leu Ala Ile Asn Val Ser Asn Tyr Asn
 305 310 315 320

Ala Trp Ser Val Ser Ser Pro Pro Pro Tyr Thr Ser Pro Asn Pro Asn
 325 330 335

Tyr Asp Glu Arg His Phe Val Glu Ala Phe Ala Pro Leu Leu Arg Gln
 340 345 350

Asn Gly Trp Asp Ala Lys Phe Ile Val Asp Gln Gly Arg Ser Gly Arg
 355 360 365

Gln Pro Thr Gly Gln Gln Glu Trp Gly His Trp Cys Asn Ala Ile Gly
 370 375 380

Thr Gly Phe Gly Gln Arg Pro Thr Ser Asn Thr Gly His Ala Asp Val
 385 390 395 400

Asp Ala Phe Val Trp Ile Lys Pro Gly Gly Glu Cys Asp Gly Thr Ser
 405 410 415

Asp Thr Ser Ala Ala Arg Tyr Asp His Phe Cys Gly Asn Pro Asp Ala
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                                         1      5

ttc act ttg cta tct ctt gcc ttg ggc tcg gcc tct gcc agc cct ttc      103
Phe Thr Leu Leu Ser Leu Ala Leu Gly Ser Ala Ser Ala Ser Pro Phe
                        10                        15                        20

ctt ctt cca agg caa gcg aac tcc tcc aac ccg ttt gct gga cac acg      151
Leu Leu Pro Arg Gln Ala Asn Ser Ser Asn Pro Phe Ala Gly His Thr
                        25                        30                        35

atc tat cca aac ccg tac tac tcc aac gag att gac gag ttt gcc att      199
Ile Tyr Pro Asn Pro Tyr Tyr Ser Asn Glu Ile Asp Glu Phe Ala Ile
                        40                        45                        50

ccc gcg ctg caa gag acc gat cct gca ctt gtg gag aag gcc gct tta      247
Pro Ala Leu Gln Glu Thr Asp Pro Ala Leu Val Glu Lys Ala Ala Leu
                        55                        60                        65

gta aaa gaa gtt gga act ttc ttc tgg att gat gtc gtc gcc aag gtc      295
Val Lys Glu Val Gly Thr Phe Phe Trp Ile Asp Val Val Ala Lys Val
70                        75                        80                        85

cca gat atc ggc cct tac ctg cag ggg atc caa gaa gca aac gcc gca      343
Pro Asp Ile Gly Pro Tyr Leu Gln Gly Ile Gln Glu Ala Asn Ala Ala
                        90                        95                        100

ggc cag aat ccg ccg tac atc ggc gcg att gtt gtc tat gac ctc ccc      391
Gly Gln Asn Pro Pro Tyr Ile Gly Ala Ile Val Val Tyr Asp Leu Pro
                        105                        110                        115

aac cgt gac tgc gct gcc gca gct tcc aac gga gag ttc agc ctc gag      439
Asn Arg Asp Cys Ala Ala Ala Ala Ser Asn Gly Glu Phe Ser Leu Glu
                        120                        125                        130

gat ggc ggc gag gag aag tac cgc ggt tat atc gac ggt atc cgg gag      487
Asp Gly Gly Glu Glu Lys Tyr Arg Gly Tyr Ile Asp Gly Ile Arg Glu
                        135                        140                        145

caa att gag aaa tac cca gac gtc cgt gtc gcg ctg gtt atc gag ccc      535
Gln Ile Glu Lys Tyr Pro Asp Val Arg Val Ala Leu Val Ile Glu Pro
150                        155                        160                        165

gat tcg ctc gcg aac atg gtc acc aat ctc aat gtc ccc aag tgc gct      583
Asp Ser Leu Ala Asn Met Val Thr Asn Leu Asn Val Pro Lys Cys Ala
                        170                        175                        180

gag tcg gag cag gct tat cga gat ggc gtc gcg tat gca ctg aaa cag      631
Glu Ser Glu Gln Ala Tyr Arg Asp Gly Val Ala Tyr Ala Leu Lys Gln
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cta gac ctc ccc aac gtc tgg aca tat atc gat gct ggt cat tca ggt      679
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tgg	ctt	ggc	tgg	ccc	gcc	aac	atc	gag	cct	gcc	gca	gaa	att	ttt	gtt		727
Trp	Leu	Gly	Trp	Pro	Ala	Asn	Ile	Glu	Pro	Ala	Ala	Glu	Ile	Phe	Val		
	215					220				225							
gag	gtc	tgg	aat	gca	gct	ggc	agg	cca	aag	tcc	act	cga	ggg	ttt	gct		775
Glu	Val	Trp	Asn	Ala	Ala	Gly	Arg	Pro	Lys	Ser	Thr	Arg	Gly	Phe	Ala		
230					235					240					245		
acg	aac	gtt	tcc	aac	tac	aac	ggg	tat	tcc	ctc	agc	acc	gct	cct	ccc		823
Thr	Asn	Val	Ser	Asn	Tyr	Asn	Gly	Tyr	Ser	Leu	Ser	Thr	Ala	Pro	Pro		
				250					255					260			
tac	act	gag	ccc	aac	ccc	aat	ttc	gac	gaa	gtg	cgt	tat	atc	aat	gca		871
Tyr	Thr	Glu	Pro	Asn	Pro	Asn	Phe	Asp	Glu	Val	Arg	Tyr	Ile	Asn	Ala		
			265					270					275				
ttc	cgc	cca	ctc	ctc	gag	gca	cgg	ggg	ttc	cca	gca	tac	ttc	atc	gtc		919
Phe	Arg	Pro	Leu	Leu	Glu	Ala	Arg	Gly	Phe	Pro	Ala	Tyr	Phe	Ile	Val		
		280					285					290					
gac	caa	ggc	cgc	agc	ggg	gtc	cag	ccc	act	gcg	cag	att	gag	caa	gga		967
Asp	Gln	Gly	Arg	Ser	Gly	Val	Gln	Pro	Thr	Ala	Gln	Ile	Glu	Gln	Gly		
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cac	tgg	tgc	aat	gtg	atc	gac	acc	ggg	ttt	gga	act	cgc	ccc	act	act		1015
His	Trp	Cys	Asn	Val	Ile	Asp	Thr	Gly	Phe	Gly	Thr	Arg	Pro	Thr	Thr		
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gac	act	ggg	aat	gag	tac	gtt	gac	tcg	atc	gtg	tgg	gtg	aag	cct	ggc		1063
Asp	Thr	Gly	Asn	Glu	Tyr	Val	Asp	Ser	Ile	Val	Trp	Val	Lys	Pro	Gly		
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ggc	gaa	tcg	gac	gga	acc	agc	gat	acc	tct	gct	gag	aga	tat	gac	tac		1111
Gly	Glu	Ser	Asp	Gly	Thr	Ser	Asp	Thr	Ser	Ala	Glu	Arg	Tyr	Asp	Tyr		
			345					350					355				
cac	tgc	gga	ctt	gag	gat	gca	ttg	aag	cca	gct	cct	gaa	gcg	gga	cag		1159
His	Cys	Gly	Leu	Glu	Asp	Ala	Leu	Lys	Pro	Ala	Pro	Glu	Ala	Gly	Gln		
		360					365					370					
tgg	ttc	cag	gcc	tac	ttc	gag	caa	ctg	ctc	aga	aat	gcc	aac	ccc	cca		1207
Trp	Phe	Gln	Ala	Tyr	Phe	Glu	Gln	Leu	Leu	Arg	Asn	Ala	Asn	Pro	Pro		
	375					380					385						
ttc	taa	atc	agat	ga	agg	acgga	ccca	attgat	gac	ggc	ctgt	cttc	gtgatc				1260
Phe																	
390																	
cgac	gaa	agc	aat	gtc	cagg	tg	aaa	atgac	cgag	agattg	gag	agtc	catg	agg	atag	gta	1320
gtca	atgatt	tc	accc	gagt	tt	ccac	gttt	tacc	ctt	ctt	gtac	atag	tt	tg	agtc	gcc	1380
tg	ttg	gtttc	ag	tag	tacat	ctt	atcc	gac	ag	agt	ctatc	gttt	gattac	ccc	agtc	aaa	1440

agcgttattg caatcttttc ctagggattt attgtttgct gcggatgtcg tggctatggg 1500
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Ser Ala Ser Pro Phe Leu Leu Pro Arg Gln Ala Asn Ser Ser Asn Pro
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Phe Ala Gly His Thr Ile Tyr Pro Asn Pro Tyr Tyr Ser Asn Glu Ile
35 40 45

Asp Glu Phe Ala Ile Pro Ala Leu Gln Glu Thr Asp Pro Ala Leu Val
50 55 60

Glu Lys Ala Ala Leu Val Lys Glu Val Gly Thr Phe Phe Trp Ile Asp
65 70 75 80

Val Val Ala Lys Val Pro Asp Ile Gly Pro Tyr Leu Gln Gly Ile Gln
85 90 95

Glu Ala Asn Ala Ala Gly Gln Asn Pro Pro Tyr Ile Gly Ala Ile Val
100 105 110

Val Tyr Asp Leu Pro Asn Arg Asp Cys Ala Ala Ala Ala Ser Asn Gly
115 120 125

Glu Phe Ser Leu Glu Asp Gly Gly Glu Glu Lys Tyr Arg Gly Tyr Ile
130 135 140

Asp Gly Ile Arg Glu Gln Ile Glu Lys Tyr Pro Asp Val Arg Val Ala
145 150 155 160

Leu Val Ile Glu Pro Asp Ser Leu Ala Asn Met Val Thr Asn Leu Asn
165 170 175

Val Pro Lys Cys Ala Glu Ser Glu Gln Ala Tyr Arg Asp Gly Val Ala

180	185	190
Tyr Ala Leu Lys Gln Leu Asp Leu Pro Asn Val Trp Thr Tyr Ile Asp		
195	200	205
Ala Gly His Ser Gly Trp Leu Gly Trp Pro Ala Asn Ile Glu Pro Ala		
210	215	220
Ala Glu Ile Phe Val Glu Val Trp Asn Ala Ala Gly Arg Pro Lys Ser		
225	230	235
Thr Arg Gly Phe Ala Thr Asn Val Ser Asn Tyr Asn Gly Tyr Ser Leu		
245	250	255
Ser Thr Ala Pro Pro Tyr Thr Glu Pro Asn Pro Asn Phe Asp Glu Val		
260	265	270
Arg Tyr Ile Asn Ala Phe Arg Pro Leu Leu Glu Ala Arg Gly Phe Pro		
275	280	285
Ala Tyr Phe Ile Val Asp Gln Gly Arg Ser Gly Val Gln Pro Thr Ala		
290	295	300
Gln Ile Glu Gln Gly His Trp Cys Asn Val Ile Asp Thr Gly Phe Gly		
305	310	315
Thr Arg Pro Thr Thr Asp Thr Gly Asn Glu Tyr Val Asp Ser Ile Val		
325	330	335
Trp Val Lys Pro Gly Gly Glu Ser Asp Gly Thr Ser Asp Thr Ser Ala		
340	345	350
Glu Arg Tyr Asp Tyr His Cys Gly Leu Glu Asp Ala Leu Lys Pro Ala		
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Pro Glu Ala Gly Gln Trp Phe Gln Ala Tyr Phe Glu Gln Leu Leu Arg		
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<223> Primer

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y is t or c
n is a, g, t, or c

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17

<210> 28
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n is a, g, t, or c

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17

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<223> n is a, g, t, or c
r is a or g

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gcnggccanc cnarcca

17

<210> 30

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n is a, g, t, or c

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y is t or c
n is a, g, t or c

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17

<210> 32
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y is t or c
n is a, g, t or c

<400> 32
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<210> 33
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25

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34

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<212> DNA
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actggattta ccatggccgg tcgattcttc c

31

<210> 36
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<400> 36
agtcacctct agttattaga aggcgggggtt g

31